

SEQUENCE LISTING

<110> Alnemri, Emad S.

<120> NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
METHODS OF USE THEREOF

<130> 480140.432D3

<140> US

<141> 2002-02-12

<160> 6

<170> PatentIn Ver. 2.0

<210> 1

<211> 1236

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1233)

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Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Leu	
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cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg ctg ttg	144
Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu	
35 40 45	
gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct ccc cag	192
Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln	
50 55 60	
cag aga gtg gcc cca caa caa aag agg tcc agc ccc tca gag gga ttg	240
Gln Arg Val Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu	
65 70 75 80	
tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc atc tcc	288
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser	
85 90 95	
tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc ctt ttc	336
Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe	
100 105 110	
tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta agt ccc	384
Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro	
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 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
 145 150 155 160

ccc aga ggg atg gtc aag gtc ggt gat tgt aca ccc tgg agt gac atc 528
 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
 165 170 175

gaa tgt gtc cac aaa gaa tca ggc atc atc ata gga gtc aca gtt gca 576
 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
 180 185 190

gcc gta gtc ttg att gtg gct gtg ttt gtt tgc aag tct tta ctg tgg 624
 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
 195 200 205

aag aaa gtc ctt cct tac ctg aaa ggc atc tgc tca ggt ggt ggt ggg 672
 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
 210 215 220

gac cct gag cgt gtg gac aga agc tca caa cga cct ggg gct gag gac 720
 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
 225 230 235 240

aat gtc ctc aat gag atc gtg agt atc ttg cag ccc acc cag gtc cct 768
 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
 245 250 255

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 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
 260 265 270

atg ttg tcc ccc ggg gag tca gag cat ctg ctg gaa cgg gca gaa gct 864
 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
 275 280 285

gaa agg tct cag agg agg agg ctg ctg gtt cca gca aat gaa ggt gat 912
 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp
 290 295 300

ccc act gag act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg 960
 Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val
 305 310 315 320

ccc ttt gac tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac 1008
 Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp
 325 330 335

aat gag ata aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc 1056
 Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr
 340 345 350

ttg tac acg atg ctg ata aag tgg gtc aac aaa acc ggg cga gat gcc 1104
 Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala
 355 360 365

tct gtc cac acc ctg ctg gat gcc ttg gag acg ctg gga gag aga ctt 1152
 Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
 370 375 380

gcc aag cag aag att gag gac cac ttg ttg agc tct gga aag ttc atg 1200
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<210> 2

<211> 411

<212> PRT

<213> Homo sapiens

<400> 2

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Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Leu
 20 25 30

Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
 35 40 45

Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
 50 55 60

Gln Arg Val Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
 65 70 75 80

Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
 85 90 95

Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
 100 105 110

Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
 115 120 125

Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
 130 135 140

Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
 145 150 155 160

Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
 165 170 175

Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala

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180 185 190
 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
 195 200 205
 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
 210 215 220
 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
 225 230 235 240
 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
 245 250 255
 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
 260 265 270
 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
 275 280 285
 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp
 290 295 300
 Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val
 305 310 315 320
 Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp
 325 330 335
 Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr
 340 345 350
 Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala
 355 360 365
 Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
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<220>
 <221> CDS
 <222> (1)..(897)

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caa Gln	gac Asp	ggc Gly 35	gtc Val	ggg Gly	aac Asn	cat His	acc Thr 40	atg Met	gcc Ala	cgg Arg	atc Ile	ccc Pro 45	aag Lys	acc Thr	cta Leu	144
aag Lys	ttc Phe 50	gtc Val	gtc Val	gtc Val	atc Ile	gtc Val 55	gcg Ala	gtc Val	ctg Leu	ctg Leu	cca Pro 60	gtc Val	cta Leu	gct Ala	tac Tyr	192
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tct Ser	cat His	aga Arg	tca Ser 100	gaa Glu	cat His	act Thr	gga Gly	gcc Ala 105	tgt Cys	aac Asn	ccg Pro	tgc Cys	aca Thr 110	gag Glu	ggt Gly	336
gtg Val	gat Asp	tac Tyr 115	acc Thr	aac Asn	gct Ala	tcc Ser	aac Asn 120	aat Asn	gaa Glu	cct Pro	tct Ser	tgc Cys 125	ttc Phe	cca Pro	tgt Cys	384
aca Thr	gtt Val 130	tgt Cys	aaa Lys	tca Ser	gat Asp	caa Gln 135	aaa Lys	cat His	aaa Lys	agt Ser	tcc Ser 140	tgc Cys	acc Thr	atg Met	acc Thr	432
aga Arg 145	gac Asp	aca Thr	gtg Val	tgt Cys	cag Gln 150	tgt Cys	aaa Lys	gaa Glu	ggc Gly	acc Thr 155	ttc Phe	cgg Arg	aat Asn	gaa Glu	aac Asn 160	480
tcc Ser	cca Pro	gag Glu	atg Met	tgc Cys 165	cgg Arg	aag Lys	tgt Cys	agc Ser	agg Arg 170	tgc Cys	cct Pro	agt Ser	ggg Gly	gaa Glu 175	gtc Val	528
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aac Asn	acc Thr 210	agc Ser	ccg Pro	ggg Gly	act Thr	cct Pro 215	gcc Ala	cca Pro	gct Ala	gct Ala	gaa Glu 220	gag Glu	aca Thr	atg Met	aac Asn	672
acc Thr 225	agc Ser	cca Pro	ggg Gly	act Thr	cct Pro 230	gcc Ala	cca Pro	gct Ala	gct Ala	gaa Glu 235	gag Glu	aca Thr	atg Met	acc Thr	acc Thr 240	720

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 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser
 245 250 255

ccg ggg act cct gcc cca gct gct gaa gag aca atg acc acc agc ccg 816
 Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro
 260 265 270

ggg act cct gcc tct tct cat tac ctc tca tgc acc atc gta ggg atc 864
 Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
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<210> 4

<211> 299

<212> PRT

<213> Homo sapiens

<400> 4

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Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro Lys Thr Leu
 35 40 45

Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro Val Leu Ala Tyr
 50 55 60

Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala
 65 70 75 80

Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly
 85 90 95

Ser His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly
 100 105 110

Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys
 115 120 125

Thr Val Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr
 130 135 140

Arg Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn
 145 150 155 160

Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val
 165 170 175

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Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu
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 Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met
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 Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn
 210 215 220
 Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
 225 230 235 240
 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser
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 Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro
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 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
 35 40 45
 gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct ccc cag 192
 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
 50 55 60
 cag aga gtg gcc cca caa caa aag agg tcc agc ccc tca gag gga ttg 240
 Gln Arg Val Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
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<210> 6
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 35 40 45
 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
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 65 70 75 80
 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
 85 90 95
 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
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 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
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 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
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 145 150 155 160
 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
 165 170 175
 Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro
 180 185 190
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 Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
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 260 265 270

Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu
 275 280 285

Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Lys Thr Gly
 290 295 300

Arg Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly
 305 310 315 320

Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly
 325 330 335

Lys Phe Met Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
 340 345 350